We claim:

1. The use of nuclear encoded Clp-protease in a method for identifying herbicides.

2. The use as claimed in claim 1, wherein the Clp-protease is

   a) selected from the group consisting of ClpP1-protease, ClpP2-protease, ClpP3-protease, ClpP4-protease and ClpP6-protease; or

   b) selected from the group consisting of ClpR1-protease, ClpR3-protease, ClpR4-protease; or

   c) ClpP-like-protease.

3. A plant nucleic acid sequence encoding a ClpP2-protease comprising:

   a) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:3, or

   b) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:4 by backtranslating, or

   c) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:3 which has an identity with SEQ ID NO:3 of has at least 66%.

4. A plant nucleic acid sequence encoding a ClpR1-protease comprising:

   a) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:11, or

   b) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:12 by backtranslating, or

   c) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:11 which has an identity with SEQ ID NO:11 of has at least 69%.

5. A plant nucleic acid sequence encoding a ClpP-like-protease comprising:

a) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:17, or

b) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:18 by backtranslating, or

c) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:17 which has an identity with SEQ ID NO:17 of has at least 67%.

6. A polypeptide with the activity of a nuclear encoded Clp-protease, encoded by a nucleic acid molecule as claimed in claim 3, 4 or 5.

7. An expression cassette comprising

a) genetic control sequences in operable linkage with a nucleic acid sequence as claimed in claim 3, 4 or 5; or

b) additional functional elements, or

c) a combination of a) and b).

8. A vector comprising an expression cassette as claimed in claim 7.

9. A transgenic organism comprising at least one nucleic acid sequence as claimed in claim 4, 5 or 6 encoding a polypeptide with the activity of a Clp-protease, an expression cassette as claimed in claim 7 or a vector as claimed in claim 8, selected from among bacteria, yeasts, fungi, animal cells or plant cells.

10. A method for identifying substances with herbicidal activity, comprising the following steps:

i. bringing a nuclear encoded Clp-protease into contact with one or more test compounds under conditions which permit the test compound(s) to bind to the nucleic acid molecule encoding Clp-protease or to the nuclear encoded Clp-protease, and

ii. detecting whether the test compound binds to the Clp-protease of i), or

iii. detecting whether the test compound reduces or blocks the enzymatic or biological activity of the Clp-protease of i), or

iv. detecting whether the test compound reduces or blocks the transcription, translation or expression of the Clp-protease of i).

11. A method as claimed in claim 10, wherein the Clp-protease is

a) selected from the group consisting of ClpP1-protease, ClpP2-protease, ClpP3-protease, ClpP4-protease and ClpP6-protease; or

b) selected from the group consisting of ClpR1-protease, ClpR3-protease, ClpR4-protease; or

c) ClpP-like-protease.

12. A method as claimed in claim 10, wherein

a) the ClpP1-protease is encoded by a nucleic acid sequence which comprises:

i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:1, or

ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:2 by back translating, or

iii) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:1 which has an identity with SEQ ID NO:1 of has at least 50%;

b) the ClpP2-protease is encoded by a nucleic acid sequence which comprises:

i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:3, or

ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:4 by back translating, or

iii) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:3 which has an identity with SEQ ID NO:3 of has at least 50%;

c) the ClpP3-protease is encoded by a nucleic acid sequence which comprises:

i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:5, or

ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:6 by back translating, or

iii) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:5 which has an identity with SEQ ID NO:5 of has at least 50%;

d) the ClpP4-protease is encoded by a nucleic acid sequence which comprises:

i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:7, or

ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:8 by back translating, or

iii) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:7 which has an identity with SEQ ID NO:7 of has at least 50%;

e) the ClpP6-protease is encoded by a nucleic acid sequence which comprises:

i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:9, or

ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:10 by back translating, or

iii) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:9 which has an identity with SEQ ID NO:9 of has at least 50%;

f) the ClpR1-protease is encoded by a nucleic acid sequence which comprises:

i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:11, or

ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:12 by back translating, or

iii) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:11 which has an identity with SEQ ID NO:11 of has at least 50%;

g) the ClpR3-protease is encoded by a nucleic acid sequence which comprises:

i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:13, or

ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:14 by back translating, or

iii) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:13 which has an identity with SEQ ID NO:13 of has at least 50%;

h) the ClpR4-protease is encoded by a nucleic acid sequence which comprises:

i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:15, or

ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:16 by back translating, or

iii) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:15 which has an identity with SEQ ID NO:15 of has at least 50%;

i) the ClpP like-protease is encoded by a nucleic acid sequence which comprises:

i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:17, or

ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:18 by back translating, or

iii) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:17 which has an identity with SEQ ID NO:17 of has at least 50%;

13. A method as claimed in claim 10, 11 or 12, wherein a test compound is selected which reduces or blocks the enzymatic or biological activity of Clp-protease.

14. A method as claimed in any of claims 10, 11, 12 or 13, wherein

i. either Clp-protease is expressed in a transgenic organism or an organism which naturally contains Clp-protease is grown,

ii. the Clp-protease of step i) is brought into contact with a test compound in the cell digest of the transgenic or nontransgenic organism, in partially purified form or in homogeneously purified form, and

iii. selecting a test compound which reduces or blocks the enzymatic activity of the Clp-protease of step a).

15. A method as claimed in any of claims 10, 11, 12 or 13, which comprises the following steps:

i. generating a transgenic organism comprising a nucleic acid sequence encoding Clp-protease, wherein Clp-protease is expressed recombinantly;

ii. applying a test substance to the transgenic organism of i) and to a non-transgenic organism of the same genotype,

iii. determining the growth or the viability of the transgenic plant and the non-transgenic plant after application of the test compound, and

iv. selecting test substances which bring about a reduced growth of the non-transgenic plant in comparison with the growth of the transgenic plant.

16. A method as claimed in claim 15, which is carried out in a plant organism, a cyanobacterium or proteobacterium.

17. A method for identifying substances with growth-regulatory activity, which comprises the following steps:

i. generating a transgenic plant comprising a nucleic acid sequence Clp-protease, wherein Clp-protease is expressed recombinantly;

ii. applying a test substance to the transgenic plant of i) and to a nontransgenic plant of the same variety,

iii. determining the growth or the viability of the transgenic plant and the nontransgenic plant after application of the test compound, and

iv. selecting test substances which bring about a reduced growth of the nontransgenic plant in comparison with the growth of the transgenic plant.

18. A method as claimed in any of claims 10 to 17, wherein the substances are identified in high-throughput screening method.

19. A support comprising one or more of the nucleic acid molecules as claimed in claim 3, 4, or 5 one or more expression cassettes as claimed in claim 7, one or more vectors as claimed in claim 8, one or more organisms as claimed in claim 9 or one or more (poly)peptides as claimed in claim 6.

20. A method as claimed in any of claims 10 to 18, wherein the substances are identified in High-Throughput Screening using a support as claimed in claim 19.

21. The use of a compound with herbicidal activity, identified by one of the methods as claimed in any of claims 10 to 16, 18 and 20 for controlling undesired vegetation and/or for regulating the growth of plants.

22. The use of a compound with growth-regulatory activity, identified by the method as claimed in any of claims 17, 18 or 20 for controlling undesired vegetation and/or for regulating the growth of plants.

23. A method for the preparation of an agrochemical composition, which comprises

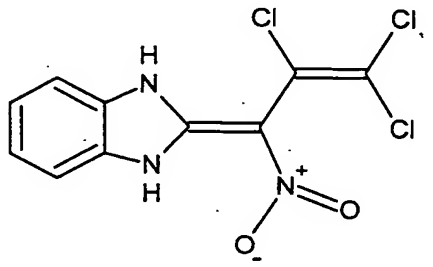
a) identifying a compound with herbicidal activity by one of the methods as claimed in any of claims 10 to 16, 18 and 20 or a compound with growth-regulatory activity as claimed in any of claims 17, 18 or 20, and

b) formulating this compound together with suitable auxiliaries to give crop protection products with herbicidal or growth-regulatory activity.

24. The use of at least one Clp-protease inhibitor identified by one of the methods as claimed in any of claims 10 to 16, 18 and 20 in a method for controlling undesired vegetation and/or for regulating the growth of plants.

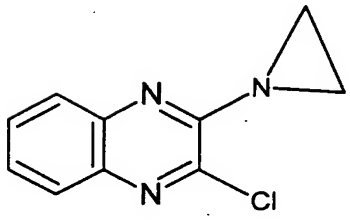
25. A method for controlling undesired vegetation and/or for regulating the growth of plants comprising treating said weeds with a herbicide, wherein said herbicide is a compound which is a inhibitor of a Clp-protease.

26. Clp-protease inhibitor of the formula:



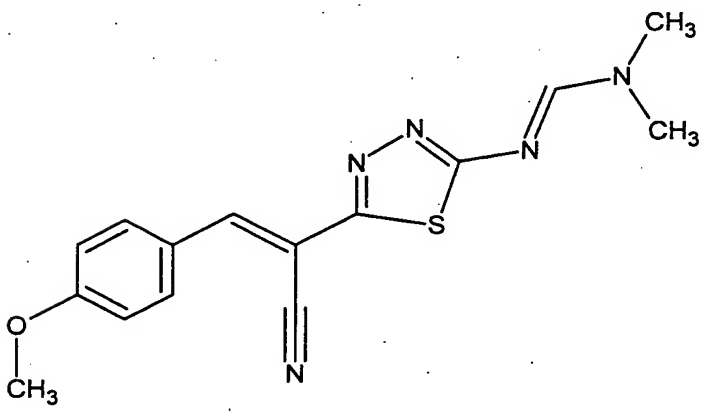
formula (I)

or



formula (II)

or



formula (III).